Amendments to the Claims

Please cancel Claim 21 and amend Claims 3, 6, 7, 11-14 and 23 as follows:

1.   (*Canceled*)

2.   (*Canceled*)

3.   (*Currently amended*) A method in a computer system for analyzing ~~an~~ and displaying data on gene expression in a molecular topography, comprising:

(a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic~~,~~ comprising a sequence identifier;

(ii)   a second value for a second polynucleotide-characteristic different from said first characteristic~~,~~ comprising a measure of size of the polynucleotide; and

(iii)   a third value that is a measure of the quantity of the polynucleotide;

(b)   calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression~~,~~

——— ~~wherein: (i) the first characteristic is a sequence identifier, and (ii) the second characteristic is a measure of size~~.

4.   (*Canceled*)

5.   (*Canceled*)

6.   (*Currently amended*) A method in a computer system for analyzing ~~an~~ and displaying data on gene expression in a molecular topography, comprising:

(a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides, wherein the polynucleotides are 3'-end fragments of restriction enzyme cleaved cDNAs or fragments thereof, the gene expression profile including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic, comprising a sequence identifier;

(ii)   a second value for a second polynucleotide-characteristic different from said first characteristic, comprising a measure of size of the polynucleotide; and

(iii)   a third value that is a measure of the quantity of the polynucleotide;

(b)   calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

~~wherein the polynucleotides are cDNAs or fragments thereof, and~~

~~wherein the polynucleotides are 3'-end fragments of restriction enzyme cleaved cDNAs.~~

7. (*Currently amended*)   The method of claim 6, wherein the first characteristic is a sequence identifier, and the second characteristic is a measure of size of the fragment.

8. (*Original*) The method of claim 7, wherein the sequence identifier is the combination of an anchor sequence of a cDNA synthesis primer and a restriction enzyme cleavage reaction specificity.

9. (*Original*) The method of claim 8, wherein values of the first and second characteristics are arranged, respectively, along first and second ordinates, the first and second ordinates defining a plane, the values of the first and second characteristics for each polynucleotide by their location on the first and second ordinates define a position in the plane, and the peak for each polynucleotide is displayed at the position of the polynucleotide on the plane.

10. (*Original*) The method of claim 9, wherein the 3' end fragments are generated by READS.

11.   (*Currently amended*) A method in a computer system for displaying differences in gene expression, comprising:

(1)   for each of ~~two gene expression profiles~~ a first gene expression profile and a second gene expression profile to be compared, generating a molecular topography according to a method in a computer system for analyzing ~~an~~ and displaying data on gene expression in a molecular topography, comprising:

(a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic,

(ii)   a second value for a second polynucleotide-characteristic different from said first characteristic, and

(iii)   a third value that is a measure of the quantity of the polynucleotide;

(b)   calculating for each polynucleotide from the first and second values a position in a two co-ordinate display space, and from the third value a peak at that position ~~in a multi-dimensional display space~~; and

(c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

(2)   for each position in the two co-ordinate display space subtracting the measure of quantity in the first gene expression profile from the measure of quantity in the second gene expression profile;

(3)   for each position, generating a peak for display from the difference; and

(4)   displaying the respective difference peak at each of the positions in the two co-ordinate display space.

12.   (*Currently amended*) A method in a computer system for displaying differences in gene expression, comprising:

(1) for each of ~~two gene expression profiles~~ a first gene expression profile and a second gene expression profile to be compared, generating a molecular topography according to a method, comprising:

(a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i) a first value for a first polynucleotide characteristic~~;~~ ;

(ii) a second value for a second polynucleotide-characteristic different from said first characteristic~~;~~ ; and

(iii) a third value that is a measure of the quantity of the polynucleotide;

(b) calculating for each polynucleotide from the first and second values a position in a two-co-ordinate display space, and from the third value calculating a peak at that position ~~in a multi-dimensional display space~~; and

(c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression~~;~~;

(2) for each position in the two co-ordinate display space subtracting the measure of quantity in the first gene expression profile from the measure of quantity in the second gene expression profile;

(3) for each position, generating a peak for display from the difference; and

(4) displaying the respective difference peak at each of the positions in the two co-ordinate display space,

wherein differences are displayed only if they meet or exceed a threshold value.

13. (*Currently amended*) A method in a computer system for comparing gene expression, comprising:

(1) for each of ~~two gene profiles~~ a first gene expression profile and a second gene expression profile to be compared, generating a molecular topography according to claim ~~1~~ 11,

(2)   for each position in the two co-ordinate <u>display</u> space subtracting a first measure of quantity in the first profile from a second measure of quantity in the second profile to generate respective difference values;

(3)   calculating from the respective difference values a measure of difference of the two profiles.

14. (*Currently amended*) The method of claim 13, wherein the first profile is a standard reference profile and the second profile is a ~~the~~ profile of a test sample.

15. (*Original*) The method of claim 14, wherein comparison of the test sample profile with the standard reference profile is diagnostic of a condition or disease.

16. (*Original*) The method of claim 15, wherein the first profile is a profile of a reference sample and the second profile is a profile of a test sample.

17. (*Original*) The method of claim 16, wherein comparison of the profile of the test sample with the profile of the reference sample is diagnostic of a condition or disease.

18. (*Original*) The method of claim 13 wherein the difference value is set to zero when the difference between the first measure and the second measure is less than two-fold.

19. (*Original*) The method of claim 13 wherein the first profile is identical to the second profile when all the respective first and second measures are identical.

20. (*Original*) The method of claim 13 wherein the first profile is similar to the second profile when the average difference between the respective first and second measures is less than a predefined amount.

21.   (*Canceled*)
22.   (*Canceled*)

23.   (*Currently amended*) A method in a computer system for displaying a series of in gene expression profiles in a molecular movie, comprising:

(1)   generating a plurality of molecular topographies according to a method, comprising:

(a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic, comprising a sequence identifier;

(ii)   a second value for a second polynucleotide-characteristic different from said first characteristic, comprising a measure of size of the polynucleotide; and

(iii)   a third value that is a measure of the quantity of the polynucleotide;

(b)   calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression; and

(2)   displaying the molecular topographies in succession;

wherein the molecular topographies are delta plots.

24.   (*Canceled*)